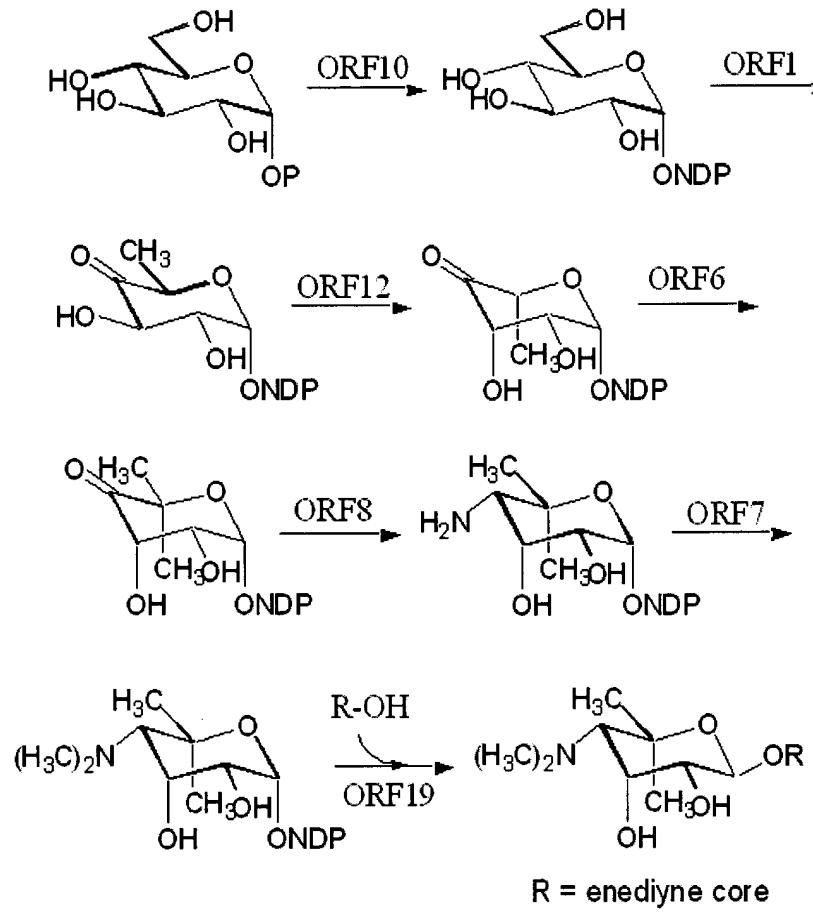


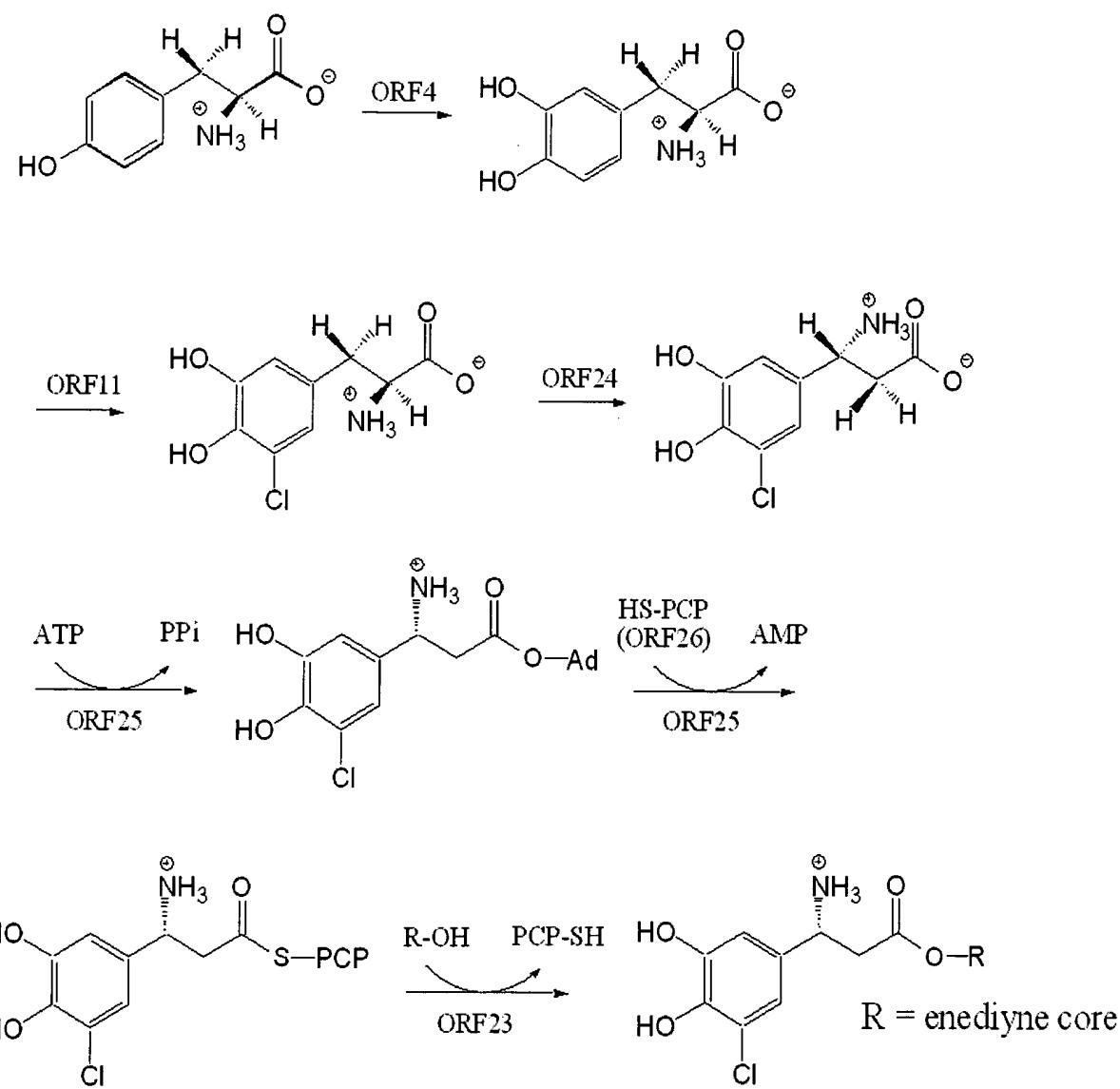
**Fig. 1**



ORF10: dNDP-glucose synthase, 355 aa  
 ORF1: dNDP-glucose dehydratase, 332 aa  
 ORF12: epimerase, 192 aa  
 ORF8: aminotransferase, 410 aa

ORF6: C-methyltransferase, 423 aa  
 ORF7: N-methyltransferase, 244 aa  
 ORF19: glycosyl transferase, 459 aa

**Fig. 2**



**ORF4: Hydroxylase, 527 aa**

**ORF11: Hydroxylase halogenase, 492/494 aa**

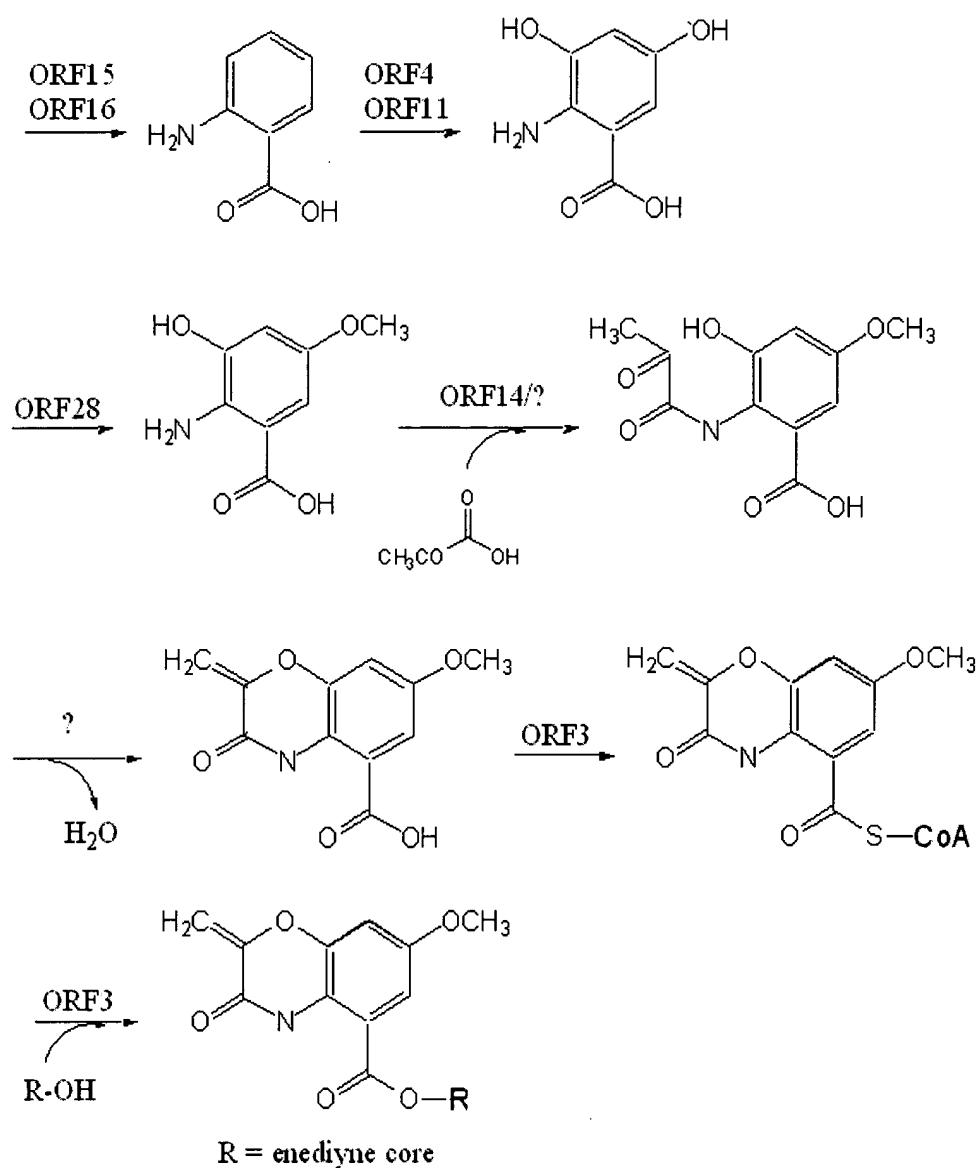
**ORF24: Aminomutase, 539 aa**

**ORF23: Type II NRPS condensation enzyme, 459 aa**

**ORF25: Type II NRPS adenylation enzyme, 716 aa**

**ORF26: Type II peptidyl carrier protein 93 aa**

**Fig. 3A**



ORF15: Anthranilate synthase I, 493 aa  
 ORF16: Anthranilate synthase II, 220 aa  
 ORF28: O-methyltransferase, 350 aa

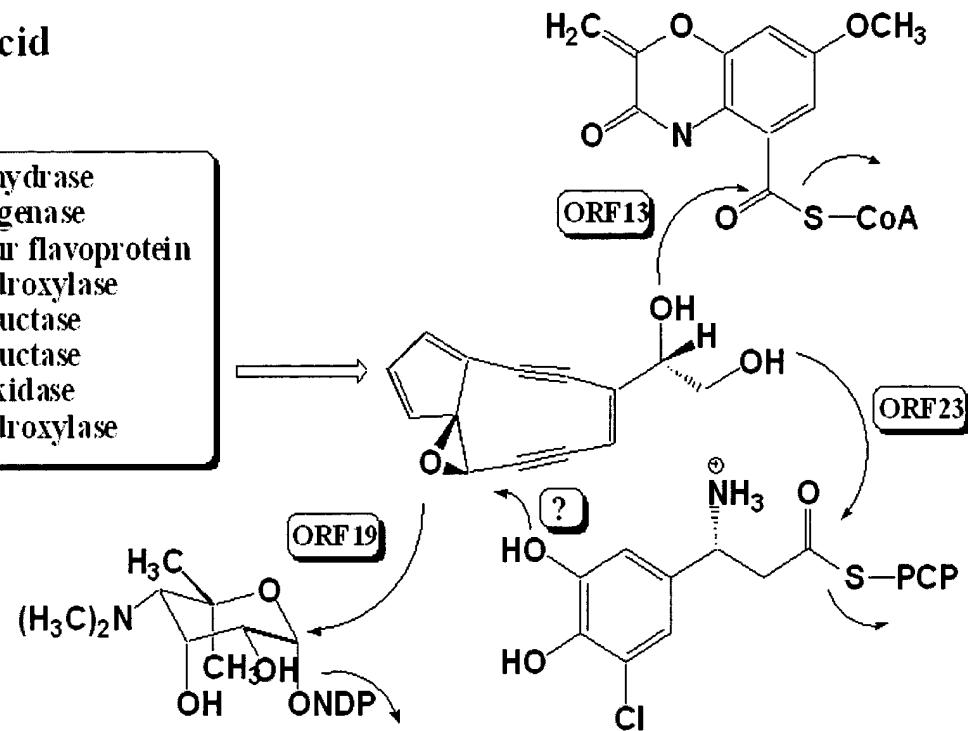
ORF3: Coenzyme F390 synthetase, 463 aa  
 ORF14: Coenzyme F390 synthetase, 484 aa  
 ORF13: O-acyltransferase, 378 aa

**Fig. 3B**



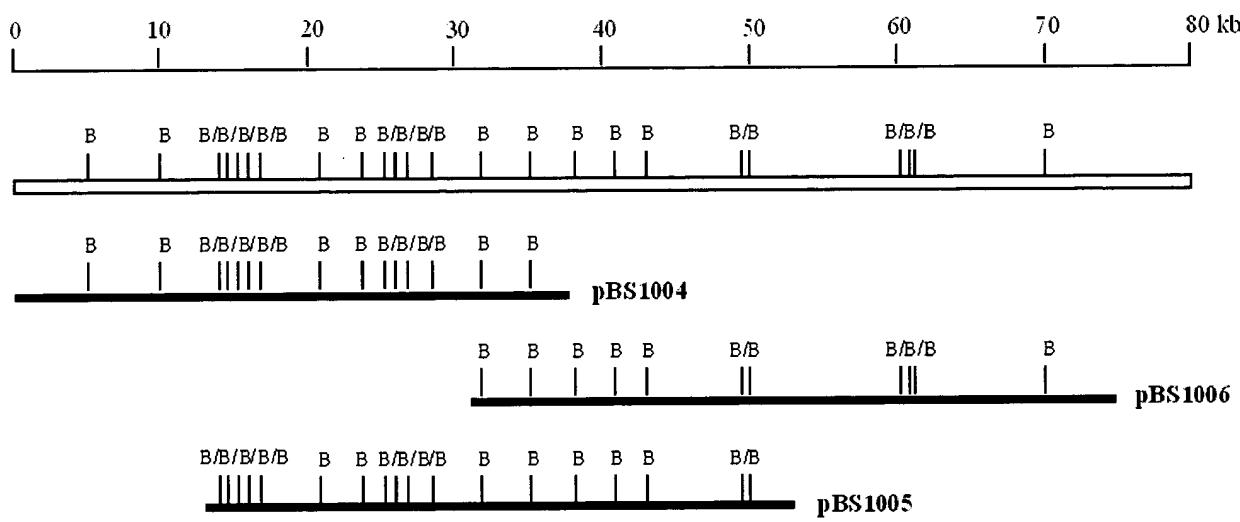
Fatty acid

ORF17: Epoxide hydrolase  
ORF20: Monooxygenase  
ORF21: Iron-sulfur flavoprotein  
ORF29: P-450 hydroxylase  
ORF30: Oxidoreductase  
ORF32: Oxidoreductase  
ORF35: Proline oxidase  
ORF38: P-450 hydroxylase

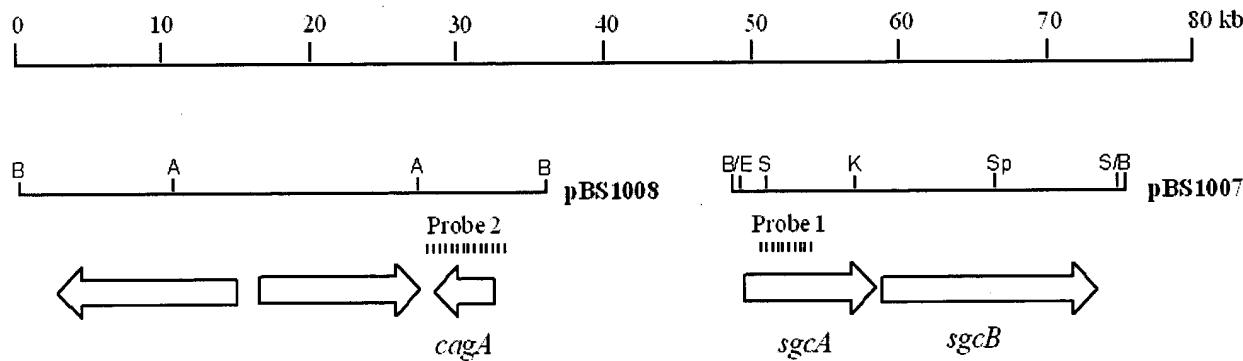


ORF13: O-acyltransferase,  
ORF19: Glycosyl transferase,  
ORF23: Type II NRPS condensation enzyme

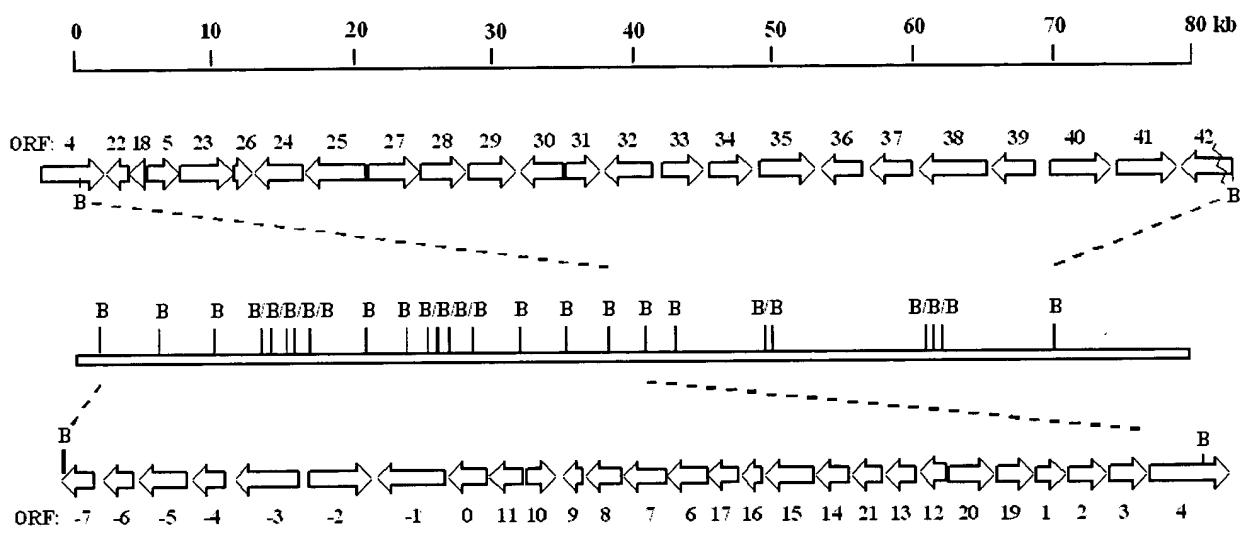
*Fig. 4*



**Fig. 5A**



**Fig. 5B**

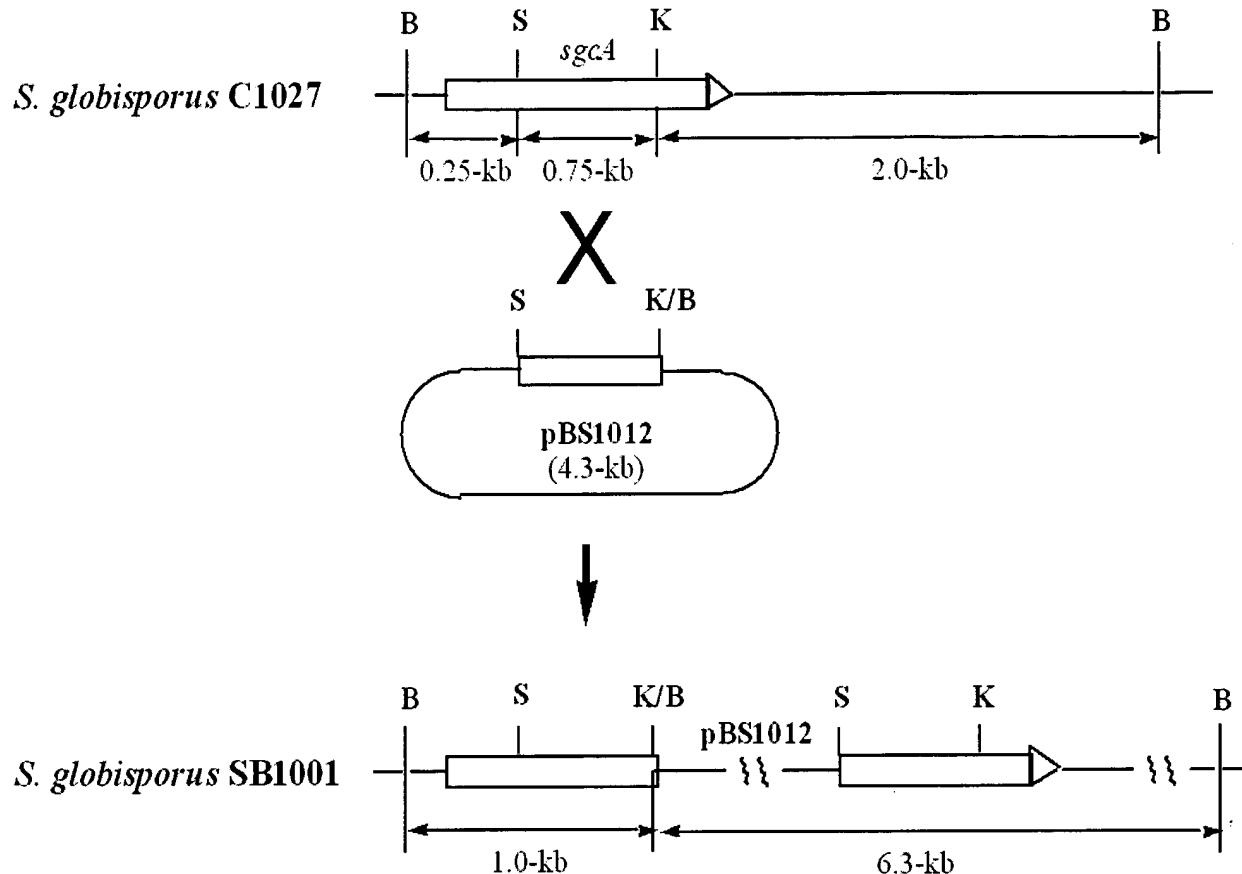


**Fig. 5C**

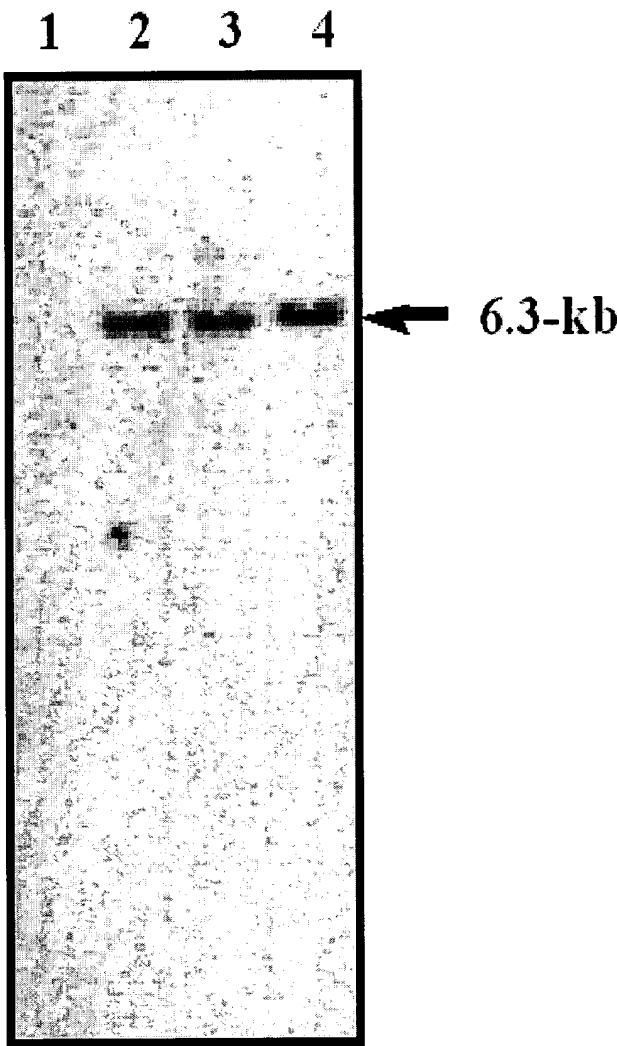


|           |                                                                                                                                       |
|-----------|---------------------------------------------------------------------------------------------------------------------------------------|
| Gdh       | 1:~~~ <b>M</b> RVLTGAGFIGSHYVROLICGGAYPAFAGADVVLDKLTYAGNEENLRPVADDPRE:                                                                |
| Ty1A2     | 1:~~~ <b>M</b> RVLTGAGFIGSHETGQLLTGAYPDIGATRTVVLDKLTYAGNPANLHVAGHPDL:                                                                 |
| SgCA      | 1:~~~ <b>M</b> RVLTGAGFIGSOEVRAHTGEELPSEDARVTVLDKLTYSGNPNALTSVAAHPRY:                                                                 |
| MtmE      | 1: <b>M</b> TTSILVTGGAGFIGSHYVRTLLIGPR..GVPDVTVTVLDKLTYAGTLTNLAEVSDSDRE:                                                              |
| consensus | 1:<br>mrVLTGGAGFIGShyvr ll g pa v VLDKLTYAg n NL va p r f : 60                                                                        |
| Gdh       | 58:R F V R G D I C E W D V Y S E V M R E V D V V V H F A A E T H V D R S I L G A S D F V V T N V V G T N T I L Q G A L A A : 117      |
| Ty1A2     | 58:R F V R G D I A D H G W W R R L M E G V G L V V H F A A E S H V D R S I E S S E A F V R T N V E G T R V I L Q A A V D A : 117      |
| SgCA      | 58:T F V Q G D T V D P R V Y D E V V A G H D V I V H F A A E S H V D R S I D T A T R F V T T N V L G T Q T I L E A A I L R H : 117    |
| MtmE      | 59:R F V R G D I C D A P L V D D L A V H D Q V V H F A A E S H V D R S I L G A A D F V R T N V F G I Q T I L L D A A I R Q : 118      |
| consensus | 61: F V r G D i d v v evm d v v V H F A A E s H V D R S I a F V T N V G T n t l l a A I : 120                                         |
| Gdh       | 118:N V S K E V H V S T D E V Y G T I E H G S W P E D H L I E P N S P Y S A A K A G S D L I T A F A Y H R T H G L B V C I T R : 177   |
| Ty1A2     | 118:G V G R E V H I S T D E V Y G S I A E G S W P E D D H E V A P N S P Y A A T K A A S D L L A I A Y H R T G L D V R V T R : 177     |
| SgCA      | 118:G V G R E V H V S T D E V Y G S I A S G S W T E D T P L A P N V P Y A A S K A G S D L M A I A T H R T G L D V V V T R : 177       |
| MtmE      | 119:G I E T E V H I S T D E V Y G S I D A G S W P E T A B V S P N S I L Y S A A K A S S D L V A L A Y H R T G L D V R V T R : 178     |
| consensus | 121:q v k F V H V S T D E V Y G S I G S W P E d p l P N S P Y A K A G S D L I A I A Y H R T H G L d v v T R : 180                     |
| Gdh       | 178:C S N N Y G P Y Q F E P K V I P L F I T N I M D G R R V P L Y G D G I N V R D W L H V T D H C R G I O L V A E S G R A G : 237     |
| Ty1A2     | 178:C S N N Y G P R O Y Q F E P K A V P L F I T N I L D G L P V P L Y G D G I N T R E W L H V D D H C R G V A L Y G A G G R P G : 237 |
| SgCA      | 178:C T N N Y G P Y Q Y P E K V I P L F V T N I L D G L R V P L Y G D G A H R R D W L H V S D H C R A T O M M N S G R A G : 237       |
| MtmE      | 179:C S N N Y G S H Q F E P K V I P L F V T S L L D G R E V P L Y G D G T N V R D W L H V D D H V R A I E L V R T G G R A G : 238     |
| consensus | 181:C s N N Y G p Q F E P K V I P L F I T n l l D G V P L Y G D G n R d W L H V D H c R g i IV G R a G : 240                          |
| Gdh       | 238:E I Y N I G G G T E L I N K E L T E R V E L M G O D W S M Q O P V T D R K G H D R R Y S V D H T K I S E E L G Y E P V : 297       |
| Ty1A2     | 238:V I Y N I G G G T E L I N A E L T D R I E L L C A D R S A L R R V A D R P G H D R R Y S V D T T K I R E E L G Y A P R : 297       |
| SgCA      | 238:E V Y H I G G G T E L S N E E L T G L L T A C G T D W S C V D R V A D R Q G H D R R Y S D I T K I R E E L G Y E P L : 297         |
| MtmE      | 239:E V Y N I G G G T E L S N K E L T Q L L D A C G A G W D R V R Y V T D R K G H D R R Y S V D C T K I R R E E L G Y R P A : 298     |
| consensus | 241:e i Y n I G G G T E L t n E L T v L e c g d w s v V D R G H D R R Y S v D T K I R E L G Y P : 300                                 |
| Gdh       | 298:V P E E R G L A E T I E W Y R D N F R A W W E P L K S A P D G G K ~ ~ ~ : 329                                                     |
| Ty1A2     | 298:T G I T E G L A G T V A W Y R D N F R A W W E P L K R S P G R E L E R A : 333                                                     |
| SgCA      | 298:V A E E D G L A A T V K W Y H E N R S w w Q P L K E A A G L L D A V G ~ : 332                                                     |
| MtmE      | 299:R E E G D A L A E T V A W Y R H H E R A W W E P L T R A Y G A V A A ~ ~ : 331                                                     |
| consensus | 301: f e g l a T v W Y r d n R a W W e P L k a g : 336                                                                                |

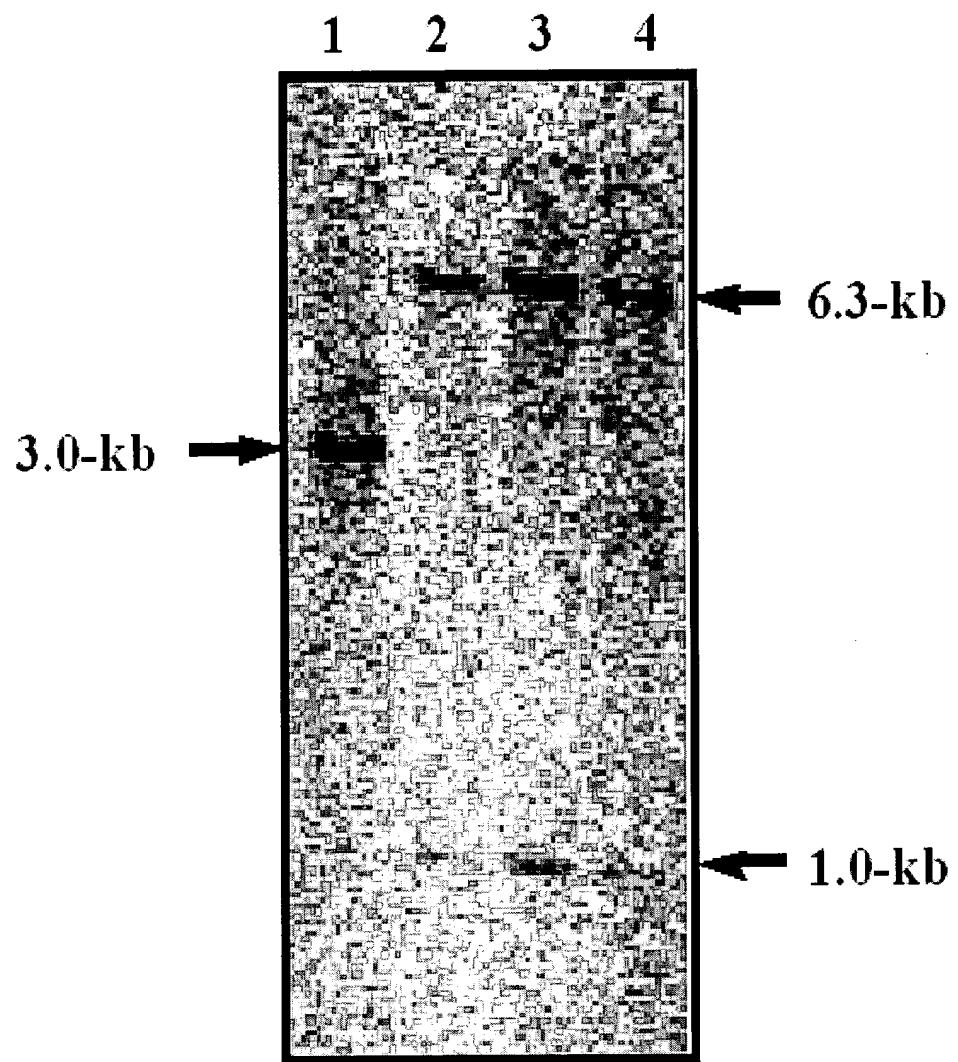
**Fig. 7**



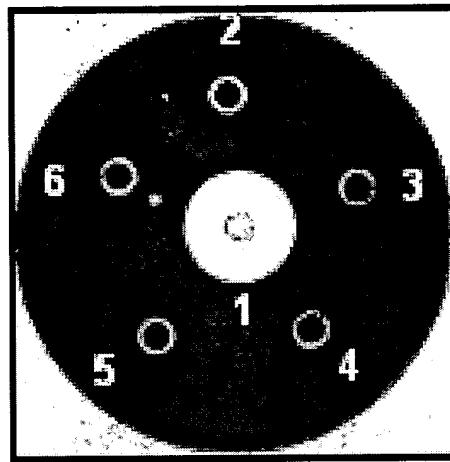
*Fig. 8A*



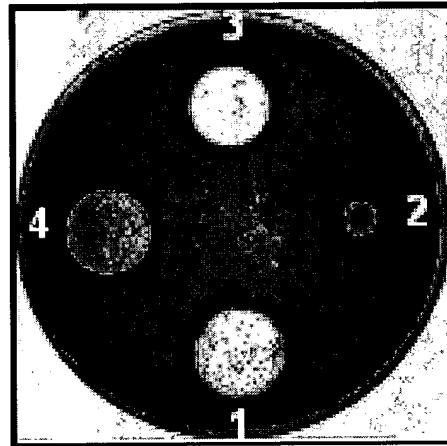
*Fig. 8B*



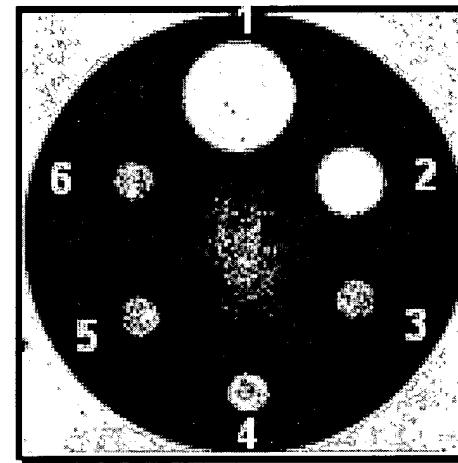
*Fig. 8C*



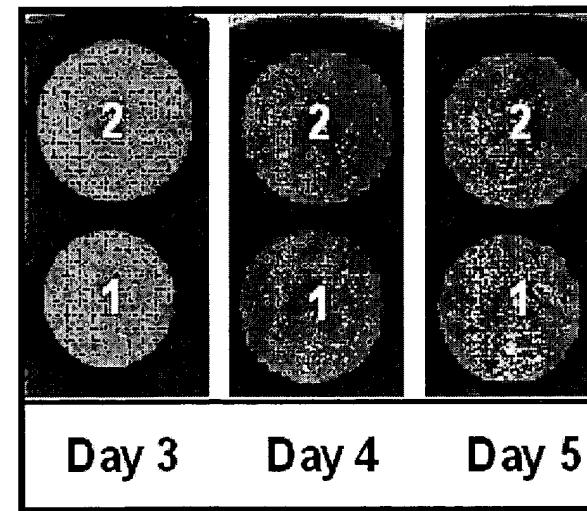
*Fig. 9A*



*Fig. 9B*



*Fig. 9C*



*Fig. 9D*

**Fig. 6**



*Fig. 6 cont'd.*